

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/869,198

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

PCT

RAW SEQUENCE LISTING

DATE: 07/09/2001

PATENT APPLICATION: US/09/869,198

TIME: 10:12:20

Input Set : A:\seqlistJAB1463PCTVegf-xseqlist.app.txt

Output Set: N:\CRF3\07092001\I869198.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Gordon, Robert
 4 Sprengel, Jorg
 5 Yon, Jeffrey
 6 Dijkmans, Josiena
 7 Gosiewska, Anna
 8 Dhanaraj, Sridevi
 9 Xu, Jean
 11 <120> TITLE OF INVENTION: Vascular Endothelial Growth Factor-X
 13 <130> FILE REFERENCE: 51935/004
 15 <140> CURRENT APPLICATION NUMBER: US/09/869,198
 16 <141> CURRENT FILING DATE: 2001-06-21
 18 <150> PRIOR APPLICATION NUMBER: GB 9828377.3
 19 <151> PRIOR FILING DATE: 1998-12-22
 21 <150> PRIOR APPLICATION NUMBER: US 60/124,967
 22 <151> PRIOR FILING DATE: 1999-03-18
 24 <150> PRIOR APPLICATION NUMBER: US 60/164,131
 25 <151> PRIOR FILING DATE: 1999-11-08
 27 <160> NUMBER OF SEQ ID NOS: 97
 29 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORED SEQUENCES

1547 <210> SEQ ID NO: 97
 1548 <211> LENGTH: 308
 1549 <212> TYPE: DNA
 1550 <213> ORGANISM: Artificial Sequence
 1552 <220> FEATURE:
 1553 <223> OTHER INFORMATION: Description of Artificial Sequence: Human EST
 1555 <400> SEQUENCE: 97
 W--> 1556 cttccattcc tggtattgga gatgaaaata aaaagcaact tatganagta gacattcaga 60
 1557 tccagccatt actaacctat tccttttttg gggaaatctg agcctagctc agaaaaacat 120
 1558 aaagcacctt gaaaaagact tggcagcttc ctgataaagc gtgctgtgct gtgcagtagg 180
 1559 aacacatcct atttattgtg atgttgtggt tttattatct taaactctgt tccatacact 240
 1560 tgtataaata catggatatt tttatgtaca gaagtatgct tcttaaccag ttcacttatt 300
 1561 gtacctgg 308
 E--> 1564 56
 E--> 1567 56

see item 9 on Error Summary Sheet

delete at end of file

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

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 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\seqlistJAB1463PCTVegf-xseqlist.app.txt

Output Set: N:\CRF3\07092001\I869198.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application Number
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:568 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:30
L:568 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:30
L:568 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:572 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:30
L:572 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:30
L:572 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:617 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:33
L:617 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:33
L:617 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:688 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:38
L:688 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:38
L:688 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:690 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:38
L:690 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:38
L:690 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:718 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:40
L:718 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:40
L:718 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:719 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:40
L:719 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:40
L:719 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:721 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:40
L:721 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:40
L:721 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:765 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:43
L:765 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:43
L:765 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:766 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:43
L:766 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:43
L:766 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:778 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:44
L:778 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:44
L:778 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:779 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:44
L:779 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:44
L:779 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:780 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:44
L:780 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:44
L:780 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:781 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:44
L:781 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:44
L:781 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:795 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:45
L:795 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:45
L:795 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:796 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:45

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Input Set : A:\seqlistJAB1463PCTVegf-xseqlist.app.txt

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L:796 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:45
L:796 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:821 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:47
L:821 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:47
L:821 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
L:850 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:49
L:850 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:49
L:850 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
L:854 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:49
L:854 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:49
L:854 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
L:880 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:51
L:880 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:51
L:880 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:884 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:51
L:884 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:51
L:884 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:930 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:54
L:930 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:54
L:930 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:1031 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:61
L:1031 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:61
L:1031 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61
L:1033 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:61
L:1033 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:61
L:1033 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61
L:1046 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:62
L:1046 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:62
L:1046 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62
L:1050 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62
L:1065 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63
L:1122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67
L:1124 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67
L:1136 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68
L:1137 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68
L:1139 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68
L:1194 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72
L:1208 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73
L:1241 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75
L:1242 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75
L:1255 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76
L:1269 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:77
L:1270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:77
L:1271 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:77
L:1272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:77
L:1284 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:78
L:1285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:78
L:1301 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:79
L:1312 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:80

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L:1313 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:80

L:1316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:80

L:1329 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81

L:1330 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81

L:1356 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83

L:1564 M:254 E: No. of Bases conflict, LENGTH:Input:56 Counted:308 SEQ:97

M:254 Repeated in SeqNo=97